

**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

(**Added material** is noted in bold underline; [deleted material] is noted in brackets)

In the Specification:

Please replace the paragraph beginning on page 4, line 17, with the following rewritten paragraph:

--OPGL is synthesised as a type II transmembrane protein consisting of 317 amino acid residues (human, cf. SEQ ID NO: 2 **(corresponding DNA sequence in SEQ ID NO: 1)**) or 316 amino acid residues (murine, cf. SEQ ID NOS: 4 and 6 **(corresponding DNA sequences in SEQ ID NOS: 3 and 5, respectively)**). Alignment of the two amino acid sequences show that identical amino acid residues are found at 87% of the homologous positions.--

Please replace the paragraph beginning on page 24, line 20, with the following rewritten paragraph:

--The promiscuous epitope can according to the invention be a naturally occurring human T-cell epitope such as epitopes from tetanus toxoid (e.g. the P2 and P30 epitopes **(SEQ ID NOS: 34 and 35, respectively)**), diphtheria toxoid, Influenza virus hemagglutinin (HA), and *P. falciparum* CS antigen. --

Please replace the paragraph beginning on page 25, line 31, with the following rewritten paragraph:

--One especially preferred PADRE peptide is the one having the amino acid sequence AKFVAAWTLKAAA (SEQ ID NO: 36) or an immunologically effective subsequence thereof. This, and other epitopes having the same lack of MHC restriction are preferred T-cell epitopes which should be present in the OPGL analogues used in the inventive method. Such super-promiscuous epitopes will allow for the most simple embodiments of the invention wherein only one single modified OPGL is presented to the vaccinated animal's immune system.--

Please replace the paragraph beginning on page 54, line 18, with the following rewritten paragraph:

--A synthetic cDNA encoding the murine OPGL residues 158-316 has been synthesized removing sub-optimal *Eschericia coli* and *Pichia pastoris* codons from the published sequence. Additionally, an N-terminal Histidine tag, part of the cleavage site of the alpha mating factor signal sequence from *Sacharomyces cerevisiae*, and suitable restriction enzymes have been incorporated into the open reading frame (cf. SEQ ID NO: 7 (corresponding amino acid sequence in SEQ ID NO: 8)).--

Please replace the paragraph beginning on page 54, line 25, with the following rewritten paragraph:

--This cDNA encoding wild type murine OPGL has been cloned into a standard *Eschericia coli* expression vector (pTrc99a) using *Bsp*HI and *Hind*III restriction enzymes and a standard cloning vector (pBluescript KS+) using

*SacI* and *KpnI* restriction enzymes (yielding SEQ ID NO: 9 (corresponding amino acid sequence in SEQ ID NO: 10)).--

Please replace the paragraph beginning on page 58, line 5, with the following rewritten paragraph:

--PCR of SEQ ID NO: 9 was performed using SEQ ID NOs: 22 and 25 as primers. The resulting PCR fragment was restriction digested with *SacII* and *KpnI* and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NO: 26 and a vector specific primer. The resulting PCR fragment was restriction digested with *KpnI* and *HindIII*. Both fragments were then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with *SacII* and *HindIII*. To correct a single base mutation in this construct, PCR using the construct as template was performed with primers SEQ ID NOs: 33 and 29. The resulting PCR fragment was restriction digested with *PstI* + *EcoRI*, gel purified and subsequently ligated to the erroneous construct digested with *PstI* and *EcoRI*. The verified construct (SEQ ID NO: 13 (corresponding amino acid sequence in SEQ ID NO: 14)) was then transferred to pTrc99a using *BspHI* and *HindIII* restriction enzymes.--

Please replace the paragraph beginning on page 58, line 23, with the following rewritten paragraph:

--PCR was performed using primers SEQ ID NOs: 27 and 28 without template. The resulting PCR fragment was restriction digested with *PstI* and *EcoRI* and subsequently purified from an agarose gel. The resulting fragment was then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with

*SacII* and *HindIII*. The verified construct (SEQ ID NO: 15 (corresponding amino acid sequence in SEQ ID NO: 16)) was subsequently transferred to pTrc99a using *BspHI* and *HindIII* restriction enzymes.--

Please replace the paragraph beginning on page 59, line 1, with the following rewritten paragraph:

--PCR of SEQ ID NO: 9 was performed using primers SEQ ID NOs: 22 and 29. The resulting PCR fragment was restriction digested with *PstI* and *BstBI* and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NO: 30 and a vector specific primer. The resulting PCR fragment was restriction digested with *BstBI* and *KpnI* and subsequently gel purified. Both fragments were then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with *PstI* and *KpnI*. The verified construct (SEQ ID NO: 17 (corresponding amino acid sequence in SEQ ID NO: 18)) was then transferred to pTrc99a using *BspHI* and *HindIII* restriction enzymes.--

Please replace the paragraph beginning on page 59, line 14, with the following rewritten paragraph:

--PCR of SEQ ID NO: 9 was performed using primers SEQ ID NOs: 22 and 23. The resulting PCR fragment was restriction digested with *SacII* and *KpnI* and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NOs: 24 and 31. The PCR fragment was restriction digested with *KpnI* and *EcoRI* and subsequently gel purified. Both fragments were then ligated to SEQ ID NO: 9 in

pBluescript KS+ restriction digested with *Sac*II and *Eco*RI. The verified construct (SEQ ID NO: 19 (corresponding amino acid sequence in SEQ ID NO: 20)) was then transferred to pTrc99a using *Bsp*HI and *Hind*III restriction enzymes.-

In the Claims:

Please replace Claim 12 with the following amended claim:

Claim 12 (amended) --The method according to claim 11, wherein the natural T-cell epitope is selected from a Tetanus toxoid epitope such as P2 or P30 (SEQ ID NOS: 34 and 35, respectively), a diphtheria toxoid epitope, an influenza virus hemagglutinin epitope, and a *P. falciparum* CS epitope.--



## SEQUENCE LISTING

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HALKIER, Torben  
HAANING, Jesper

<120> Method for Down-Regulating Osteoprotegerin Ligand  
Activity

<130> 3631-0108P

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 Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys  
 100 105 110 115  
 agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa 562  
 Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln  
 120 125 130  
 cac att gtg ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa 610  
 His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu  
 135 140 145  
 ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag gcc cag cca 658  
 Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro  
 150 155 160  
 ttt gca cac ctc acc atc aat gct gcc agc atc cca tcg ggt tcc cat 706  
 Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His  
 165 170 175  
 aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg gcc aag atc 754  
 Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile  
 180 185 190 195

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tct aac atg acg tta agc aac gga aaa cta agg gtt aac caa gat ggc 802
Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly
200 205 210
ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat gaa aca tcg 850
Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser
215 220 225
gga agc gta cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa 898
Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys
230 235 240
acc agc atc aaa atc cca agt tct cat aac ctg atg aaa gga ggg agc 946
Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser
245 250 255
acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat tcc ata aat 994
Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn
260 265 270 275
gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att agc att cag 1042
Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln
280 285 290
gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg acg tac ttt 1090
Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe
295 300 305
ggg gct ttc aaa gtt cag gac ata gac tga gactcatttc gtggaacatt 1140
Gly Ala Phe Lys Val Gln Asp Ile Asp
310 315
agcatggatg tcctagatgt ttggaaactt cttaaaaaat ggatgatgtc tatacatgtg 1200
taagactact aagagacatg gccacgggtg tatgaaactc acagccctct ctcttgagcc 1260
tgtacagggt gtgtatatgt aaagtccata ggtgatgtta gattcatggt gattacacaa 1320
cggttttaca attttgtaat gatttcctag aattgaacca gattgggaga ggtattccga 1380
tgcttatgaa aaacttacac gtgagctatg gaaggggggc acagtctctg ggtctaacc 1440
ctggacatgt gccactgaga accttgaaat taagaggatg ccatgtcatt gcaaagaaat 1500
gatagtgtga aggggttaagt tcttttgaat tgttacattg cgctgggacc tgcaaataag 1560
ttcttttttt ctaatgagga gagaaaaata tatgtatttt tatataatgt ctaaagttat 1620
atttcagggtg taatgttttc tgtgcaaagt tttgtaaatt atatttgtgc tatagtattt 1680
gattcaaaat atttaaaaaat gtctcactgt tgacatatatt aatgttttaa atgtacagat 1740
gtattttaact ggtgcacttt gtaattcccc tgaagggtact cgtagctaag ggggcagaat 1800
actgtttctg gtgaccacat gtagtttatt tctttattct ttttaactta atagagtctt 1860
cagacttgtc aaaactatgc aagcaaaaaa aataaaaata aataaaaata ataccttgaa 1920
taataagtag gatgttggtc accagggtgcc tttcaaattt agaagctaag tgacttttagg 1980
agctgacata gccaaaaagg atacataata ggctactgaa atctgtcagg agtattttatg 2040
caattattga acagggtgtc ttttttacaa gagctacaaa ttgtaaattt tgtttctttt 2100
ttttcccata gaaaatgtac tatagtttat cagccaaaaa acaatccact ttttaattta 2160
gtgaaagtta ttttattata ctgtacaata aaagcattgt ctctgaatgt taattttttg 2220
gtacaaaaaa taaatttgta cgaaaacctg aaaaaaaaaa aaaaaaaggg cggccgctct 2280
agagggccct attctatag 2299

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<210> 6
<211> 316
<212> PRT
<213> Mus musculus

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<400> 6
Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
1 5 10 15
Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
20 25 30
Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser

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<221> misc\_feature  
 <222> (1)..(36)  
 <223> C-terminal part of *Saccharomyces cerevisiae*  
         alpha-mating factor  
  
 <220>  
 <221> misc\_feature  
 <222> (85)..(561)  
 <223> Encoding wild type murine OPGL, residues 158-316

<400> 7  
 gag ctc gga tcc ctc gag aaa aga gag gct gaa gct cat gtc atg aaa 48  
 Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys  
     1                    5                    10                    15  
 cac caa cac caa cat caa cat caa cat caa cat caa aaa cct gaa gct 96  
 His Gln His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala  
                     20                    25                    30  
 cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct tct ggt 144  
 Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly  
             35                    40                    45  
 tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt tgg gct 192  
 Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala  
     50                    55                    60  
 aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt aac cag 240  
 Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln  
     65                    70                    75                    80  
 gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat cac gaa 288  
 Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu  
             85                    90                    95  
 acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt tac gtt 336  
 Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val  
             100                    105                    110  
 gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg aaa ggt 384  
 Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly  
             115                    120                    125  
 ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc tac tct 432  
 Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser  
     130                    135                    140  
 atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc tct 480  
 Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser  
     145                    150                    155                    160  
 atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct acc 528  
 Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr  
             165                    170                    175  
 tac ttc ggg gcc ttc aaa gtt cag gac atc gac tag 564  
 Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
             180                    185

<210> 8  
 <211> 187  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR  
         product with optimum codons for *E. coli* and *P.*

pastoris expression

<400> 8

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Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys
 1           5           10           15
His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala
 20           25           30
Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
 35           40           45
Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala
 50           55           60
Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
 65           70           75           80
Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
 85           90           95
Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
100           105           110
Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
115           120           125
Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
130           135           140
Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
145           150           155           160
Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
165           170           175
Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
180           185

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<210> 9

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA encoding  
murine OPGL, residues 158-316, fused to His tag

<220>

<221> CDS

<222> (1)..(519)

<220>

<221> misc\_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc\_feature

<222> (43)..(519)

<223> Murine OPGL, residues 158-316

<400> 9

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atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct      48
Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1           5           10           15
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct  96

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Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
			20					25					30			
tct	ggt	tct	cat	aaa	ggt	acc	ctg	tct	tct	tgg	tat	cac	gac	cgc	ggt	144
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
		35					40					45				
tgg	gct	aaa	atc	tct	aac	atg	acc	ctg	tct	aac	ggt	aaa	ctg	aga	ggt	192
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
	50					55				60						
aac	cag	gac	ggt	ttc	tac	tac	ctg	tac	gct	aac	atc	tgt	ttc	aga	cat	240
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
	65			70					75						80	
cac	gaa	acc	tct	ggt	tct	ggt	cca	acc	gac	tac	ctg	cag	ctg	atg	ggt	288
His	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	
			85					90					95			
tac	ggt	ggt	aaa	acc	tct	atc	aaa	atc	cca	tct	tca	cat	aac	ctg	atg	336
Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
			100					105				110				
aaa	ggt	ggt	tct	acc	aaa	aac	tgg	tct	ggt	aac	tct	gaa	ttc	cat	ttc	384
Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
		115					120					125				
tac	tct	atc	aac	ggt	ggt	ggt	ttc	ttc	aaa	ctg	aga	gct	ggt	gaa	gaa	432
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	
	130				135					140						
atc	tct	atc	cag	ggt	tct	aac	cct	tct	ctg	ctg	gac	cca	gac	cag	gac	480
Ile	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
	145			150					155						160	
gct	acc	tac	ttc	ggg	gcc	ttc	aaa	ggt	cag	gac	atc	gac				519
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp				
			165					170								

<210> 10

<211> 173

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA encoding  
murine OPGL, residues 158-316, fused to His tag

<400> 10

Met	Lys	His	Gln	His	Gln	His	Gln	His	Gln	His	Gln	His	Gln	Lys	Pro	
	1			5				10						15		
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
			20					25					30			
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
		35					40				45					
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
	50					55				60						
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
	65			70					75						80	
His	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	
			85					90					95			
Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
			100					105					110			
Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
		115					120					125				



Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu
130						135					140				
Ile	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp
145					150					155					160
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp			
				165					170						

<210> 11

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of murine OPGL, residues 158-316 with C to S mutation, and His tag

<220>

<221> CDS

<222> (1)..(519)

<220>

<221> misc\_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc\_feature

<222> (43)..(228)

<223> Murine OPGL, residues 158-219

<220>

<221> misc\_feature

<222> (232)..(519)

<223> Murine OPGL, residues 221-316

<220>

<221> mutation

<222> (229)..(231)

<223> tgt (Cys) to tcc (Ser)

<220>

<400> 11

atg	aaa	cac	caa	cac	caa	cat	caa	cat	caa	cat	caa	cat	caa	aaa	cct	48
Met	Lys	His	Gln	His	Gln	His	Gln	His	Gln	His	Gln	His	Gln	Lys	Pro	
1				5				10					15			
gaa	gct	cag	cca	ttc	gct	cat	ctg	acc	atc	aac	gct	gca	tcg	atc	cct	96
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
			20				25					30				
tct	ggt	tct	cat	aaa	gtt	acc	ctg	tct	tct	tgg	tat	cac	gac	cgc	ggt	144
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
		35				40					45					
tgg	gct	aaa	atc	tct	aac	atg	acc	ctg	tct	aac	ggt	aaa	ctg	aga	gtt	192
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
	50					55					60					

aac cag gac ggt ttc tac tac ctg tac gct aac atc tcc ttc aga cat	240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His	
65 70 75 80	
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt	288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
85 90 95	
tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg	336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met	
100 105 110	
aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc	384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe	
115 120 125	
tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa	432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu	
130 135 140	
atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac	480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
145 150 155 160	
gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac	519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
165 170	

<210> 12

<211> 173

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of  
murine OPGL, residues 158-316 with C to S  
mutation, and His tag

<400> 12

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro	
1 5 10 15	
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	
20 25 30	
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	
35 40 45	
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val	
50 55 60	
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His	
65 70 75 80	
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
85 90 95	
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met	
100 105 110	
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe	
115 120 125	
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu	
130 135 140	
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
145 150 155 160	
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
165 170	

<210> 13  
 <211> 564  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion of  
 murine OPGL, residues 158-316 modified by  
 introduction of tetanus toxoid P30 epitope, and  
 His tag

<220>  
 <221> CDS  
 <222> (1)..(564)

<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(336)  
 <223> Murine OPGL, residues 158-255

<220>  
 <221> misc\_feature  
 <222> (337)..(399)  
 <223> Tetanus toxoid P30 epitope

<220>  
 <221> misc\_feature  
 <222> (400)..(564)  
 <223> Murine OPGL, residues 262-316

<400> 13  
 atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80  
 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95  
 tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336  
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met

100	105	110	
ttc aac aac ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct			384
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser			
115	120	125	
gct tct cac ctg gaa aac tgg tct ggt aac tct gaa ttc cat ttc tac			432
Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr			
130	135	140	
tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc			480
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile			
145	150	155	160
tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct			528
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala			
165	170	175	
acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac			564
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp			
180	185		

<210> 14  
 <211> 188  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion of  
 murine OPGL, residues 158-316 modified by  
 introduction of tetanus toxoid P30 epitope, and  
 His tag

<400> 14  
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95  
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
 100 105 110  
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
 115 120 125  
 Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr  
 130 135 140  
 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile  
 145 150 155 160  
 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
 165 170 175  
 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 180 185

<210> 15

<211> 546  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 between murine OPGL, residues 158-316 with tetanus  
 toxoid P2 epitope introduced, and His tag

<220>  
 <221> CDS  
 <222> (1)..(546)

<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(336)  
 <223> Murine OPGL, residues 158-255

<220>  
 <221> misc\_feature  
 <222> (382)..(546)  
 <223> Murine OPGL, residues 262-316

<220>  
 <221> misc\_feature  
 <222> (337)..(381)  
 <223> Tetanus toxoid P2 epitope

<400> 15  
 atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80  
 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95  
 tac gtt gtt aaa acc cct atc aaa atc caa tct tca cat aac ctg atg 336  
 Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met  
 100 105 110  
 cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg aac 384  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn

	115		120		125		
tgg tct ggt aac tct gaa ttc cat ttc tac tct atc aac gtt ggt ggt						432	
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly							
130		135		140			
ttc ttc aaa ctg aga gct ggt gaa gaa atc tct atc cag gtt tct aac						480	
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn							
145		150		155		160	
cct tct ctg ctg gac cca gac cag gac gct acc tac ttc ggg gcc ttc						528	
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe							
	165		170		175		
aaa gtt cag gac atc gac						546	
Lys Val Gln Asp Ile Asp							
	180						

<210> 16

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
between murine OPGL, residues 158-316 with tetanus  
toxoid P2 epitope introduced, and His tag

<400> 16

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro	
1 5 10 15	
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	
20 25 30	
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	
35 40 45	
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val	
50 55 60	
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	
65 70 75 80	
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
85 90 95	
Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met	
100 105 110	
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn	
115 120 125	
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly	
130 135 140	
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn	
145 150 155 160	
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe	
165 170 175	
Lys Val Gln Asp Ile Asp	
180	

<210> 17

<211> 519

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion between  
 murine OPGL, residues 158-316 with tetanus toxoid  
 P2 epitope introduced, and His tag

<220>  
 <221> CDS  
 <222> (1)..(519)

<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(432)  
 <223> Murine OPGL, residues 158-287

<220>  
 <221> misc\_feature  
 <222> (478)..(519)  
 <223> Murine OPGL, residues 303-316

<220>  
 <221> misc\_feature  
 <222> (433)..(477)  
 <223> Tetanus toxoid P2 epitope

<400> 17  
 atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 65 70 75 80  
 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288  
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val  
 85 90 95  
 tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336  
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
 100 105 110  
 aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384  
 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
 115 120 125  
 tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
 130 135 140

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cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg gac 480
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
145          150          155          160
gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
          165          170

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<210> 18  
 <211> 173  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion between  
 murine OPGL, residues 158-316 with tetanus toxoid  
 P2 epitope introduced, and His tag

```

<400> 18
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
 1          5          10          15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
          20          25          30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
          35          40          45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
          50          55          60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
          65          70          75          80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
          85          90          95
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
          100          105          110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
          115          120          125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
          130          135          140
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
          145          150          155          160
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
          165          170

```

<210> 19  
 <211> 519  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion between  
 murine OPGL, residues 158-316 with tetanus toxoid  
 P30 epitope introduced, and His tag

<220>  
 <221> CDS  
 <222> (1)..(519)



<220>  
 <221> misc\_binding  
 <222> (1)..(42)  
 <223> His tag

<220>  
 <221> misc\_feature  
 <222> (43)..(231)  
 <223> Murine OPGL, residues 158-220

<220>  
 <221> misc\_feature  
 <222> (295)..(519)  
 <223> Murine OPGL, residues 242-316

<220>  
 <221> misc\_feature  
 <222> (232)..(294)  
 <223> Tetanus toxoid P30 epitope

<400> 19  
 atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48  
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro  
 1 5 10 15  
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96  
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro  
 20 25 30  
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144  
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly  
 35 40 45  
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192  
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val  
 50 55 60  
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aac aac 240  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn  
 65 70 75 80  
 ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct gct tct cac 288  
 Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His  
 85 90 95  
 ctg gaa gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336  
 Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met  
 100 105 110  
 aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384  
 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe  
 115 120 125  
 tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu  
 130 135 140  
 atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480  
 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 145 150 155 160  
 gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 165 170

<210> 20



<400> 22  
 ctcatctgac catcaacgct gcat 24

<210> 23  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR primer

<400> 23  
 tttcgggtacc ctccagccaga aagaaacggt gaagttgttg aaacagatgt tagcgtacag 60  
 gtag 64

<210> 24  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR primer

<400> 24  
 tgagggtacc gaaagtttct gcttctcacc tggaagttaa aaccctatc aaaatccaat 60  
 c 61

<210> 25  
 <211> 63  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR primer

<400> 25  
 tttcgggtacc ctccagccaga aagaaacggt gaagttgttg aacatcaggt tatgtgaaga 60  
 ttg 63

<210> 26  
 <211> 62  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic PCR primer

<400> 26  
 tgagggtacc gaaagtttct gcttctcacc tggaaaactg gtctggtaac tctgaattcc 60

<210> 27  
<211> 79  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 27  
tacctgcagc tgatggttta cgttgttaaa acccctatca aaatccaatc ttcacataac 60  
ctgatgcagt acatcaaag 79

<210> 28  
<211> 83  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 28  
tggaattcag agttaccaga ccagttcagt tcggtgatac cgatgaattt cgaattagct 60  
ttgatgtact gcatcaggtt atg 83

<210> 29  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 29  
gaatttcgaa ttagctttga tgtactgttc ttcaccagct ctcagtttg 49

<210> 30  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 30  
gctaattcga aattcatcgg tatcaccgaa ctggacgcta cctacttcgg ggc 53

<210> 31  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 31  
cttactagtc gatgtcctga actttg 26

<210> 32  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 32  
agtggaattc agagttacca gaccagtttt tggtagaacc acctttcatc aggttatgtg 60  
aagatgggat ttg 74

<210> 33  
<211> 65  
<212> DNA  
<213> Clostridium tetani

<400> 33  
actacctgca gctgatggtt tacgttggtt aaacctctat caaaatccca tcttcacata 60  
acctg 65

<210> 34  
<211> 15  
<212> PRT  
<213> Clostridium tetani

<400> 34  
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
1 5 10 15

<210> 35  
<211> 21  
<212> PRT  
<213> Clostridium tetani

<400> 35  
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
1 5 10 15  
Ala Ser His Leu Glu  
20

<210> 36  
<211> 13  
<212> PRT  
<213> Artificial Sequence

*210*  
*Cont*  
<220>  
<223> A pan DR epitope ("PADRE") peptide

<400> 36  
Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala  
1 5 10

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